

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT:
(A) NAME: Mitotix, Inc.
(B) STREET: One Kendall Square, Building 600
(C) CITY: Cambridge
(D) STATE: MA
10 (E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02139
(G) TELEPHONE: (617) 225-0001
(H) TELEFAX: (617) 225-0005
- 15 (ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
Human Pathogens, and Uses Related Thereto
- (iii) NUMBER OF SEQUENCES: 12

- 20 (iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII (text)
- 25 (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/463,090
(B) FILING DATE: 05-JUN-1995

30 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1668 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- 40 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 259..1491

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATGATACA AATGTGGAAG ATGCAAATTG TTCTTCCCCT ACTTTGATGA GAAAAAGTGC 60

50 ATTGAGTAAA ATCATCTTCA AAGGACATTA AACAATAATT CCAAATCACC ATCGCCAACT 120

TTTTCAAATA CAAATGCAAC ATCTGGCTCT CCATTGTCAA ATCTTTCTCG TGCACCATTG 180

AGAAATTTAT CTAATTTTCGT TATTCCTTCG TCAGTTAAAT CAAAAACGAA ACAATTTACA 240

55 AACTCTTTGA CTCGTTCA ATG ACT GAA GTG GTT TCG AAA TCA TCA CAC TCA 291

Met Thr Glu Val Val Ser Lys Ser Ser His Ser

1 5 10

	TTT	TTC	AAT	AAT	TTG	CAT	CTT	GCA	ACC	TCA	ACT	GCG	TCT	TCT	TCA	GTA	339
	Phe	Phe	Asn	Asn	Leu	His	Leu	Ala	Thr	Ser	Thr	Ala	Ser	Ser	Ser	Val	
				15					20					25			
5	TCG	AGC	ACA	ACT	CCC	AAA	ATA	GAA	TTC	AAT	TCC	ATA	GCT	GAA	AAT	GAT	387
	Ser	Ser	Thr	Thr	Pro	Lys	Ile	Glu	Phe	Asn	Ser	Ile	Ala	Glu	Asn	Asp	
			30					35					40				
10	GAT	ATC	CCT	ACC	AAT	TAT	GAC	TCT	GAT	GAA	GAA	TTC	GAA	GAT	GGT	GAT	435
	Asp	Ile	Pro	Thr	Asn	Tyr	Asp	Ser	Asp	Glu	Glu	Phe	Glu	Asp	Gly	Asp	
		45					50					55					
15	ACG	TTT	ATA	CAA	TCC	ACC	TTG	ATT	CAC	CAG	TTC	AAC	GCA	AGT	CAA	GTA	483
	Thr	Phe	Ile	Gln	Ser	Thr	Leu	Ile	His	Gln	Phe	Asn	Ala	Ser	Gln	Val	
	60					65					70					75	
20	ACA	ACA	ACA	ACA	ATA	ATA	ATA	ATA	CCA	ATG	ATG	GTA	ACG	ACA	ATA	ATA	531
	Thr	Thr	Thr	Thr	Ile	Ile	Ile	Ile	Pro	Met	Met	Val	Thr	Thr	Ile	Ile	
					80					85					90		
	TAC	CTA	CAA	AAA	TTA	GAC	GGT	TCC	ACT	CCA	TGT	ACC	AAA	CCG	ATA	AAG	579
	Tyr	Leu	Gln	Lys	Leu	Asp	Gly	Ser	Thr	Pro	Cys	Thr	Lys	Pro	Ile	Lys	
				95				100						105			
25	AGA	TTG	CAT	CGT	ACC	AAC	TTC	ATG	AAG	ATA	ATT	CAT	TTT	GAA	ATT	TAC	627
	Arg	Leu	His	Arg	Thr	Asn	Phe	Met	Lys	Ile	Ile	His	Phe	Glu	Ile	Tyr	
			110					115					120				
30	AAT	ATT	GAA	TAT	TCT	CAT	CTG	GAG	AGT	GAT	TTG	TTA	CCA	CGA	ATC	GAT	675
	Asn	Ile	Glu	Tyr	Ser	His	Ser	Glu	Ser	Asp	Leu	Leu	Pro	Arg	Ile	Asp	
		125					130					135					
35	GCT	CAT	CAA	TTA	GCC	AGA	ATA	TTA	CGT	GGA	GAC	CAC	GAT	GAC	CAA	TTT	723
	Ala	His	Gln	Leu	Ala	Arg	Ile	Leu	Arg	Gly	Asp	His	Asp	Asp	Gln	Phe	
	140					145					150					155	
40	GAT	GAA	TTT	ATT	ATC	ATT	GAT	TGT	CGA	TTT	GAG	TAT	GAA	TTT	AAT	GGT	771
	Asp	Glu	Phe	Ile	Ile	Ile	Asp	Cys	Arg	Phe	Glu	Tyr	Glu	Phe	Asn	Gly	
				160				165							170		
	GGC	CAT	ATT	ACT	AGG	GCA	ATC	AAT	ATC	TCC	ACC	CAG	GAA	GCA	CTT	CAA	819
	Gly	His	Ile	Thr	Arg	Ala	Ile	Asn	Ile	Ser	Thr	Gln	Glu	Ala	Leu	Gln	
				175				180						185			
45	GAA	AAG	CTC	TTT	CAA	TAT	CAA	GAA	ACA	GAT	ACC	AAG	GAC	ACT	GAA	AGC	867
	Glu	Lys	Leu	Phe	Gln	Tyr	Gln	Glu	Thr	Asp	Thr	Lys	Asp	Thr	Glu	Ser	
			190					195					200				
50	AAG	AAG	CGA	TTG	ATA	ATT	TTC	CAT	TGT	GAG	TTC	AGT	ATG	TTC	AGA	GGA	915
	Lys	Lys	Arg	Leu	Ile	Ile	Phe	His	Cys	Glu	Phe	Ser	Met	Phe	Arg	Gly	
		205					210					215					
55	CCA	ATG	ATG	GCC	AAA	CAT	TTA	AGA	AAG	TGT	GAT	AGA	ATG	TGC	AAC	TAC	963
	Pro	Met	Met	Ala	Lys	His	Leu	Arg	Lys	Cys	Asp	Arg	Met	Cys	Asn	Tyr	
	220					225					230					235	
	GAC	AAT	TAT	CCT	CTA	TTA	ACA	TAC	CCC	GAT	ATT	GCA	ATT	TTG	GAA	GGA	1011
	Asp	Asn	Tyr	Pro	Leu	Leu	Thr	Tyr	Pro	Asp	Ile	Ala	Ile	Leu	Glu	Gly	
				240						245				250			

	GGC TAT AAG AAT TTC TAT GAA AAT TAC CCC CAA TGG TGT GAT CCT CAA	1059
	Gly Tyr Lys Asn Phe Tyr Glu Asn Tyr Pro Gln Trp Cys Asp Pro Gln	
	255 260 265	
5	GGA TAT GTC GAG ATG AAG AAT TTA CGA CAC AAA AAA TTA TGT GAA TCC	1107
	Gly Tyr Val Glu Met Lys Asn Leu Arg His Lys Lys Leu Cys Glu Ser	
	270 275 280	
10	AAC TTG GAT AAA GTT AGA AAA GAT AAT AAA CTA ACT AGA GCA AAG TCT	1155
	Asn Leu Asp Lys Val Arg Lys Asp Asn Lys Leu Thr Arg Ala Lys Ser	
	285 290 295	
15	TAT CAA TTT GGT ATT CAA CAC CGC CGT GGT GGT TCC ACT GGT GGA CTT	1203
	Tyr Gln Phe Gly Ile Gln His Arg Arg Gly Gly Ser Thr Gly Gly Leu	
	300 305 310 315	
20	TTC GGC AAC TAT AAT TAC AAC GTT ATG AAC TCA TCA GAT CAA CAA TTT	1251
	Phe Gly Asn Tyr Asn Tyr Asn Val Met Asn Ser Ser Asp Gln Gln Phe	
	320 325 330	
	TGG AGT AGC AGT ACT TCC AAC ACT GCT CAC CAC AGA AGT AGT AGC AGT	1299
	Trp Ser Ser Ser Thr Ser Asn Thr Ala His His Arg Ser Ser Ser Ser	
	335 340 345	
25	AGC GGG TTC ATT AAT AAT ATG CAT AGT GGT GCT TCG TCA TAT CAC CAT	1347
	Ser Gly Phe Ile Asn Asn Met His Ser Gly Ala Ser Ser Tyr His His	
	350 355 360	
30	AGG TCA CAA TCG TTT GTA ACT ATC AAT AAT GAG AAA ATT ATC AAG CGA	1395
	Arg Ser Gln Ser Phe Val Thr Ile Asn Asn Glu Lys Ile Ile Lys Arg	
	365 370 375	
35	CAA AGA TCG ACT CCC AAA GTC AGC AAC TCA CCA ACC AAG CCA CCT CAT	1443
	Gln Arg Ser Thr Pro Lys Val Ser Asn Ser Pro Thr Lys Pro Pro His	
	380 385 390 395	
40	CAA CTG TAT CTC CTG ATA AAC CCA TTC CGT TGG CTA ATA TTC ATA GAT	1491
	Gln Ser Tyr Leu Ser Ile Asn Pro Phe Arg Trp Leu Ile Phe Ile Asp	
	400 405 410	
	TAACTCGTGC CAACACTATT TCATCAGACC AAACATTGTT TAGCAATAAG CTGGTATCTT	1551
45	CCCCAATGAT ATCTCCACTT GCAGCTAGTT TTGAACAATC GTCGATTGGA ATAAGTTCTT	1611
	CTGAATTATC AGTCAATACT CAAGATTTTC AACCACCGAC TACGTCCTTT AGGAATT	1668

(2) INFORMATION FOR SEQ ID NO:2:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 786 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - 55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(A) NAME/KEY: CDS
(B) LOCATION: 208..513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	AACTTGTTTA CTTATTTGTT TATATAATTG ATAGATATCA ATTACTAATT TACCCTTGTT	60
10	TTTTACTTCC TACTATTCAA GACTTTATTT CCTCCTGATA ATCATTTTGT TTGATTATCA	120
	TTTTCGTCAA TTAGTTCTTT TTTTTCATTT GTTCCAGAG TTTAGGAAGA CTACCATTTT	180
15	ACAATTTTCA ATTCAAATAT TTTCCCA ATG ACT AAA CCA AGA TTT TTA ACA Met Thr Lys Pro Arg Phe Leu Thr	231
	1 5	
20	AGA TAT AGA AAG AGC AAA AGT GTT GGA ATT TCA GAT ATG ATC CAT TAC Arg Tyr Arg Lys Ser Lys Ser Val Gly Ile Ser Asp Met Ile His Tyr	279
	10 15 20	
25	AGT CCC AGA TAC AGT GAT GAT TCA TAC GAG TAT AGA CAT GTG ATG TTA Ser Pro Arg Tyr Ser Asp Asp Ser Tyr Glu Tyr Arg His Val Met Leu	327
	25 30 35 40	
30	CCC AAG AAT ATG TTG AAA GCA ATT CCT CAC GAT TAC TTT AAT CAA GAA Pro Lys Asn Met Leu Lys Ala Ile Pro His Asp Tyr Phe Asn Gln Glu	375
	45 50 55	
35	ACA GGT ACT TTG AGG ATA TTG ACA GAA GAA GAA TGG AGA GGG TTA GGA Thr Gly Thr Leu Arg Ile Leu Thr Glu Glu Glu Trp Arg Gly Leu Gly	423
	60 65 70	
40	ATC ACA CAA TCT TTG GGT TGG GCC CAT TAC GAA ACT CAT GCT CCA GAG Ile Thr Gln Ser Leu Gly Trp Ala His Tyr Glu Thr His Ala Pro Glu	471
	75 80 85	
45	CCT CAT ATA TTA TTA TTC AAG AGA CCC TTA AAT CCC GGG CAA Pro His Ile Leu Leu Phe Lys Arg Pro Leu Asn Pro Gly Gln	513
	90 95 100	
50	TAAAAAGATT AACTATATTT GAATACTATA GAATCGGAAT CGGTTTTAAA GTTAACACTG	573
	GAATTAAAAC ATAAAAAGGA AAGAAATAGC CCATTGGTCA CAGTAATCTG TTTCCAACAA	633
	CCCCCCTCCT CAGAAATAGG ATAGAAATGA ATTAACGATG AATTTGTATA CACTATTTAT	693
	AAGCCAATCT CATTGATTGC ATTTCTTATT TGTATATTAT TAAATACGTA TATCGCGAGA	753
	AACTGTATAA ATACTCTTGG TACCTCGCAT GTT	786

55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1002 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

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5      (ix) FEATURE:
          (A) NAME/KEY: CDS
          (B) LOCATION: 43..993

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10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAGAACACAC ACATCCCAAG CCAAGACCAA CACTTATTGC AA ATG GTA GAG TTA 54
Met Val Glu Leu
1

15

TCT	GAT	TAT	CAA	CGT	CAA	GAA	AAA	GTC	GGA	GAA	GGT	ACT	TAT	GGG	GTT	102
Ser	Asp	Tyr	Gln	Arg	Gln	Glu	Lys	Val	Gly	Glu	Gly	Thr	Tyr	Gly	Val	
5					10					15					20	

20	GTT TAT AAA GCA TTA GAT ACC AAG CAC AAT AAT AGA GTT GTT GCA TTA	150
	Val Tyr Lys Ala Leu Asp Thr Lys His Asn Asn Arg Val Val Ala Leu	
	25 30 35	

25 AAG AAA ATT CGA TTA GAA TCA GAA GAT GAA GGT GTA CCT AGT ACC GCC 198
Lys Lys Ile Arg Leu Glu Ser Glu Asp Glu Gly Val Pro Ser Thr Ala
 40 45 50

ATT AGA GAA ATC TCG TTA TTA AAA GAA ATG AAA GAT GAT AAT ATC GTT 246
Ile Arg Glu Ile Ser Leu Leu Lys Glu Met Lys Asp Asp Asn Ile Val

30 55 60 65

CGA TTA TAT GAT ATT ATT CAT TCA GAT TCT CAT AAA TTA TAT TTA GTA 294
Arg Leu Tyr Asp Ile Ile His Ser Asp Ser His Lys Leu Tyr Leu Val
70 75 80

35

TTT	GAA	TTT	TTG	GAT	TTA	GAT	TTA	AAG	AAA	TAT	ATG	GAA	AGT	ATT	CCT	342
Phe	Glu	Phe	Leu	Asp	Leu	Asp	Leu	Lys	Lys	Tyr	Met	Glu	Ser	Ile	Pro	
85					90					95					100	

40 CAA GGA GTT GGA CTA GGG GCT AAT ATG ATA AAA AGA TTT ATG AAT CAA 390
Gln Gly Val Gly Leu Gly Ala Asn Met Ile Lys Arg Phe Met Asn Gln
105 110 115

TTA ATT CGA GGT ATT AAA CAT TGT CAT TCT CAT CGA GTT TTA CAT CGT 438
Leu Ile Arg Gly Ile Lys His Cys His Ser His Arg Val Leu His Arg

120 125 130

50 GAT TTA AAA CCA CAA AAT TTA TTG ATT GAT AAA GAA GGG AAT TTA AAA 486
 Asp Leu Lys Pro Gln Asn Leu Leu Ile Asp Lys Glu Gly Asn Leu Lys
 135 140 145

TTA GCA GAT TTT GGA TTA GCT CGA GCA TTT GGA GTT CCA TTA AGA GCA 534
Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Leu Arg Ala
150 155 160

55 TAT ACT CAT GAA GTT GTC ACT TTA TGG TAT CGA GCT CCC GAA ATC TTG 582
Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu
165 170 175 180

	TTA GGA GGG AAA CAA TAT TCC ACT GGG GTA GAT ATG TGG TCT GTT GGA	630
	Leu Gly Gly Lys Gln Tyr Ser Thr Gly Val Asp Met Trp Ser Val Gly	
	185 190 195	
5	TGT ATA TTT GCT GAA ATG TGT AAT AGG AAA CCA TTA TTT CCT GGT GAT	678
	Cys Ile Phe Ala Glu Met Cys Asn Arg Lys Pro Leu Phe Pro Gly Asp	
	200 205 210	
10	TCA GAA ATT GAT GAA ATT TTC CGA ATT TTC CGA ATT TTA GGA ACA CCT	726
	Ser Glu Ile Asp Glu Ile Phe Arg Ile Phe Arg Ile Leu Gly Thr Pro	
	215 220 225	
15	AAT GAA GAA ATT TGG CCT GAT GTT AAT TAT TTA CCA GAT TTT AAA TCA	774
	Asn Glu Glu Ile Trp Pro Asp Val Asn Tyr Leu Pro Asp Phe Lys Ser	
	230 235 240	
20	AGT TTC CCT CAA TGG AAA AAG AAA CCT TTG AGT GAA GCA GTT CCA AGT	822
	Ser Phe Pro Gln Trp Lys Lys Lys Pro Leu Ser Glu Ala Val Pro Ser	
	245 250 255 260	
25	TTG GAT GCT AAT GGA ATT GAT CTT TTG GAT CAA ATG TTG GTG TAT GAT	870
	Leu Asp Ala Asn Gly Ile Asp Leu Leu Asp Gln Met Leu Val Tyr Asp	
	265 270 275	
30	CCA AGT AGA AGA ATA AGT GCT AAA CGA GCT TTA ATT CAT CCT TAT TTT	918
	Pro Ser Arg Arg Ile Ser Ala Lys Arg Ala Leu Ile His Pro Tyr Phe	
	280 285 290	
35	AAT GAT AAT GAT GAT CGT GAT CAT AAC AAT TAT AAT GAA GAT AAT ATT	966
	Asn Asp Asn Asp Asp Arg Asp His Asn Asn Tyr Asn Glu Asp Asn Ile	
	295 300 305	
40	GGG ATT GAC AAA CAC CAA AAC ATG CAA TAAATCTTG	1002
	Gly Ile Asp Lys His Gln Asn Met Gln	
	310 315	

(2) INFORMATION FOR SEQ ID NO:4:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

50 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 184..1659

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTATTCCCC CCTTTCCTT TTTTATATAG AGAACTTAT TCCAATTACT CATCGAACAA	60
GATCTTACTA GACTTGTAGA CTCACGACAC GATAAATTTT AATTCATTAA TCAACCAACG	120

	AACCAGCCAA	ACCAAAATTA	ATTCACATTT	ATACTCACTG	TTTGTCATTT	TCATCTCATA	180
5	GTA ATG CCA CAA GTC ACT AAA ACT AAT AAT GAA AAT GAG TTT AGA CTT Met Pro Gln Val Thr Lys Thr Asn Asn Glu Asn Glu Phe Arg Leu 1 5 10 15	228					
10	ACT AGA TCA AAA GTA CAG CAT CAA GAG TCG ATA AGT ACC ATC AAA AAT Thr Arg Ser Lys Val Gln His Gln Glu Ser Ile Ser Thr Ile Lys Asn 20 25 30	276					
15	ACG ACC ATA TCC AAT TCT CAG CAT AAA CAA CAA ACA CAA CAA CAA ATT Thr Thr Ile Ser Asn Ser Gln His Lys Gln Gln Thr Gln Gln Gln Ile 35 40 45	324					
20	TCA TCA CCA CCT CAA GTC TCT GTA ACA TCA TCT GAA GGA GTT TCA CAT Ser Ser Pro Pro Gln Val Ser Val Thr Ser Ser Glu Gly Val Ser His 50 55 60	372					
25	GTC AAT ACA CGT CAA TAT TTG GGT GAT GTT TCA AAT CAA TAC ATA ACA Val Asn Thr Arg Gln Tyr Leu Gly Asp Val Ser Asn Gln Tyr Ile Thr 65 70 75	420					
30	AAT GCT AAA CCA ACA AAT AAA AGA AAA CCA TTG GGT GGA GAC AAT GCC Asn Ala Lys Pro Thr Asn Lys Arg Lys Pro Leu Gly Gly Asp Asn Ala 80 85 90 95	468					
35	CCT CTA CAA AAA CAA CAG CAT AGA CCA TCT AGA CCA ATA CCC ATT GCC Pro Leu Gln Lys Gln Gln His Arg Pro Ser Arg Pro Ile Pro Ile Ala 100 105 110	516					
40	AGT GAT AAC AAC AAT AAT GGT AGT ACC AGT AGC AGT AGC AAC AGT AGC Ser Asp Asn Asn Asn Asn Gly Ser Thr Ser Ser Ser Ser Asn Ser Ser 115 120 125	564					
45	AAC AAC AAT AAC AAC GAC GCA AAT AGA CTA GCA TCT TTG GCA GTT CCA Asn Asn Asn Asn Asn Asp Ala Asn Arg Leu Ala Ser Leu Ala Val Pro 130 135 140	612					
50	TCT CGA TTA CCC CAA AAA CGA CAA GCT ACT GAA TCG TCG ACA AAT TTA Ser Arg Leu Pro Gln Lys Arg Gln Ala Thr Glu Ser Ser Thr Asn Leu 145 150 155	660					
55	GTA GAG AAA TTA AGA GTA CCA CAA CCA GAA GTA GGG GAA AGA AGT CAG Val Glu Lys Leu Arg Val Pro Gln Pro Glu Val Gly Glu Arg Ser Gln 160 165 170 175	708					
60	TCA TAC CAT AAG AAA TCA CGT TTA ATT GAT TAT GAA TGG CAG GAT TTG Ser Tyr His Lys Lys Ser Arg Leu Ile Asp Tyr Glu Trp Gln Asp Leu 180 185 190	756					
65	GAT GAA GAA GAT AAT GAC GAC CAA TTA ATG GTT AGT GAA TAT GTT AAC Asp Glu Glu Asp Asn Asp Asp Gln Leu Met Val Ser Glu Tyr Val Asn 195 200 205	804					
70	GAA ATA TTT TCG TAC TAT TAC GAA TTA GAA ACA CGA ATG TTA CCT GAT Glu Ile Phe Ser Tyr Tyr Tyr Glu Leu Glu Thr Arg Met Leu Pro Asp 210 215 220	852					
75	CCG CAA TAT CTT TTC AAA CAA ACA TTG TTA AAA CCA AGA ATG AGA TCG	900					

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	Pro 225	Gln 225	Tyr 225	Leu 225	Phe 225	Lys 225	Gln 230	Thr 230	Leu 230	Leu 230	Lys 230	Pro 235	Arg 235	Met 235	Arg 235	Ser 235	
5	ATA Ile 240	TTG Leu 240	GTT Val 240	GAT Asp 240	TGG Trp 240	CTT Leu 245	GTT Val 245	GAA Glu 245	ATG Met 245	CAT His 245	TTA Leu 250	AAA Lys 250	TTC Phe 250	AAG Lys 250	TTA Leu 255	TTA Leu 255	948
10	CCT Pro 260	GAA Glu 260	TCA Ser 260	CTT Leu 260	TTT Phe 260	TTG Leu 265	GCA Ala 265	GTC Val 265	AAT Asn 265	GTA Val 265	ATG Met 265	GAT Asp 270	AGA Arg 270	TTC Phe 270	ATG Met 270	TCT Ser 270	996
15	GTT Val 275	GAA Glu 275	GTG Val 275	GTT Val 275	CAA Gln 275	ATA Ile 280	GAT Asp 280	AAA Lys 280	TTA Leu 280	CAA Gln 280	TTA Leu 285	TTG Leu 285	GCT Ala 285	ACA Thr 285	GCA Ala 285	GCT Ala 285	1044
20	TTA Leu 290	TTT Phe 290	ACT Thr 290	GCT Ala 290	GCC Ala 295	AAA Lys 295	AAT Asn 295	GAA Glu 295	GAA Glu 295	GTA Val 295	TTT Phe 300	TCT Ser 300	CCC Pro 300	CTG Ser 300	GTT Val 300	AAA Lys 300	1092
25	AAT Asn 305	TAT Tyr 305	GCA Ala 305	TAT Tyr 305	TTC Phe 310	ACT Thr 310	GAT Asp 310	GGT Gly 310	TCA Ser 315	TAT Tyr 315	ACT Thr 315	CCA Pro 315	GAA Glu 315	GAA Glu 315	GTG Val 315	GTA Val 315	1140
30	CAA Gln 320	GCA Ala 320	GAA Glu 320	AAA Lys 320	TAC Tyr 325	ATG Met 325	CTT Leu 325	ACC Thr 325	ATT Ile 325	CTT Leu 330	AAC Asn 330	TTT Phe 330	GAT Asp 330	TTG Leu 335	AAT Asn 335	TAC Tyr 335	1188
35	CCC Pro 340	AAT Asn 340	CCA Pro 340	ATG Met 340	AAT Asn 340	TTC Phe 345	TTG Leu 345	AGA Arg 345	AGA Arg 345	ATT Ile 345	TCT Ser 345	AAA Lys 350	GCT Ala 350	GAT Asp 350	GAT Asp 350	TAT Tyr 350	1236
40	GAT Asp 355	GTC Val 355	CAA Gln 355	TCA Ser 355	AGA Arg 360	ACG Thr 360	CTA Leu 360	GGA Gly 360	AAA Lys 360	TAT Tyr 365	CTT Leu 365	TTG Leu 365	GAA Glu 365	ATC Ile 365	ACT Thr 365	ATA Ile 365	1284
45	GTT Val 370	GAT Asp 370	TAC Tyr 370	AAA Lys 370	TTT Phe 375	ATT Ile 375	GGT Gly 375	ATG Met 375	AGA Arg 375	CCA Pro 380	TCT Ser 380	TTA Leu 380	TGT Cys 380	TGT Cys 380	GCC Ala 380	CTG Ser 380	1332
50	GCC Ala 385	ATG Met 385	TAT Tyr 385	TTA Leu 390	GCA Ala 390	AGA Arg 390	CTA Leu 390	ATA Ile 395	TTG Leu 395	GGC Gly 395	AAA Lys 395	TTG Leu 395	CCA Pro 395	GTT Val 395	TGG Trp 395	AAT Asn 395	1380
55	GGG Gly 400	AAT Asn 400	TTG Leu 400	ATT Ile 400	CAT His 405	TAT Tyr 405	AGT Ser 405	GGA Gly 410	GGT Gly 410	TAT Tyr 410	AGA Arg 410	ATC Ile 410	AGT Ser 410	GAT Asp 415	ATG Met 415	AGA Arg 415	1428
60	GAA Glu 420	TGT Cys 420	ATC Ile 420	GAA Glu 420	TTA Leu 420	ATG Met 425	TTT Phe 425	CAA Gln 425	TAT Tyr 425	CTT Leu 425	ATT Ile 425	GCT Ala 430	CCT Pro 430	ATA Ile 430	GAA Glu 430	CAT His 430	1476
65	GAT Asp 435	GAA Glu 435	TTT Phe 435	TTC Phe 435	AAA Lys 440	AAA Lys 440	TAT Tyr 440	GCC Ala 440	ATG Met 440	AGA Arg 445	AAA Lys 445	TTT Phe 445	ATG Met 445	AGA Arg 445	GCA Ala 445	AGT Ser 445	1524
70	ACT Thr 450	CTT Leu 450	TGT Cys 450	CGA Arg 450	AAT Asn 455	TGG Trp 455	GCT Ala 455	AAA Lys 455	AAA Lys 455	TTC Phe 460	CAA Gln 460	GCA Ala 460	TCA Ser 460	GGA Gly 460	AGA Arg 460	GAT Asp 460	1572

TTG TTT GAT GAA CGA TTA TCG ACC CAT AGG CTA ACA TTA GAA GAT GAT 1620
Leu Phe Asp Glu Arg Leu Ser Thr His Arg Leu Thr Leu Glu Asp Asp
465 470 475

5 GAC GAA GAA GAA GAA ATA GTG GTA GCA GAA GCA GAA GAG TAAAGTTTGT 1669
Asp Glu Glu Glu Glu Ile Val Val Ala Glu Ala Glu Glu
480 485 490

10 AGGACTATTG GATCTAGGTT CTTATCTTTA CAATGCATAA ATGAGGAAAT GAAAGAAGAT 1729
GAACATGAGT TATGTGCATT ACC 1752

15 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1070 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 30..1058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATCAAATCCA TCAGAGAACC ACATCAATC ATG TCT ACT GCA GCA GTT GCA ACG 53
Met Ser Thr Ala Ala Val Ala Thr
1 5

35 AAA CCA TCT GTC ACT TCA AAA CCA GCA ACT AAA CAA GTT CTG AAT TAC 101
Lys Pro Ser Val Thr Ser Lys Pro Ala Thr Lys Gln Val Leu Asn Tyr
10 15 20

40 ACC AAA GAA AAA AAA GTA GGG GAA GGT ACA TAT GCT GTT GTG TAC TTG 149
Thr Lys Glu Lys Lys Val Gly Glu Gly Thr Tyr Ala Val Val Tyr Leu
25 30 35 40

45 GGT AAA CAA ATC TCC ACC AAA CGT CAA ATT GCC ATC AAA GAA ATC AAA 197
Gly Lys Gln Ile Ser Thr Lys Arg Gln Ile Ala Ile Lys Glu Ile Lys
45 50 55

50 ACA GGA TTA TTC AAA GAT GGG TTG GAT ATG TCA GCA TTG AGA GAA GTG 245
Thr Gly Leu Phe Lys Asp Gly Leu Asp Met Ser Ala Leu Arg Glu Val
60 65 70

55 AAA TAT TTG CAA GAA TTG AAA CAT CCC AAT GTT ATT GAA CTA GTA GAT 293
Lys Tyr Leu Gln Glu Leu Lys His Pro Asn Val Ile Glu Leu Val Asp
75 80 85

GTA TTT TCA GCA ACA AAT AAT TTA AAT TTG GTA TTA GAA TTT CTA CCT 341
Val Phe Ser Ala Thr Asn Asn Leu Asn Leu Val Leu Glu Phe Leu Pro
90 95 100

0002220000

5	TGC Cys 105	GAT Asp	TTG Leu	GAA Glu	GTG Val	TTG Leu	ATC Ile	AAA Lys	GAT Asp	AAA Lys	TCG Ser	ATT Ile	GTT Val	TTC Phe	AAA Lys	TCA Ser	389
						110					115					120	
10	GCA Ala	GAT Asp	ATC Ile	AAA Lys	TCA Ser	TGG Trp	CTT Leu	TTA Leu	ATG Met	ACA Thr	TTA Leu	CGT Arg	GGG Gly	ATA Ile	CAT His	CAT His	437
					125				130						135		
15	TGT Cys	CAT His	CGG Arg	AAT Asn	TTT Phe	ATT Ile	TTA Leu	CAT His	CGT Arg	GAT Asp	TTG Leu	AAA Lys	CCA Pro	AAT Asn	AAT Asn	TTA Leu	485
				140					145					150			
20	TTA Leu	TTG Leu	GCA Ala	CCG Pro	GAT Asp	GGA Gly	CAA Gln	TTG Leu	AAA Lys	ATA Ile	GCG Ala	GAT Asp	TTT Phe	GGT Gly	CTT Leu	GCA Ala	533
			155				160						165				
25	CGA Arg	GCT Ala	TTG Leu	GTA Val	AAT Asn	CCT Pro	AAT Asn	GAA Glu	GAT Asp	TTA Leu	TCA Ser	TCT Ser	AAT Asn	GTT Val	GTC Val	ACT Thr	581
		170					175					180					
30	AGA Arg	TGG Trp	TAT Tyr	AGA Arg	GCC Ala	CCT Pro	GAA Glu	TTA Leu	TTA Leu	TTT Phe	GGT Gly	GCT Ala	CGA Arg	CAT His	TAC Tyr	ACT Thr	629
	185					190					195					200	
35	GGA Gly	GCA Ala	GTT Val	GAT Asp	ATC Ile	TGG Trp	TCA Ser	ATA Ile	GGT Gly	ATA Ile	ATA Ile	TTT Phe	GCT Ala	GAA Glu	TTA Leu	ATG Met	677
				205				210						215			
40	CTT Leu	CGA Arg	ATA Ile	CCT Pro	TAT Tyr	TTG Leu	CCA Pro	GGT Gly	AAA Lys	GAT Asp	GAC Asp	GTT Val	GAT Asp	CAA Gln	TTA Leu	GAT Asp	725
				220				225						230			
45	GTT Val	ACA Thr	TTT Phe	AGA Arg	GCT Ala	TAT Tyr	GGG Gly	ACA Thr	CCA Pro	ACA Thr	GAG Glu	CAA Gln	ATA Ile	TGG Trp	CCA Pro	AAT Asn	773
			235				240					245					
50	GTT Val	TCC Ser	AGT Ser	TTG Leu	CCA Pro	ATG Met	TAT Tyr	AAT Asn	GCA Ala	CTT Leu	CAT His	GTG Val	TAT Tyr	CCA Pro	CCT Pro	CCT Pro	821
		250				255						260					
55	TCA Ser	AGA Arg	CAA Gln	GAA Glu	TTA Leu	CGT Arg	AAT Asn	AGA Arg	TTT Phe	AGT Ser	GCT Ala	GCT Ala	ACG Thr	GAA Glu	AAA Lys	GCC Ala	869
	265					270					275					280	
60	CTT Leu	GAT Asp	TTG Leu	TTG Leu	ATA Ile	TCG Ser	ATG Met	ACC Thr	CAA Gln	TTG Leu	GAT Asp	CCA Pro	AGT Ser	AGA Arg	AGA Arg	TGT Cys	917
					285				290					295			
65	GAT Asp	TCT Ser	ACA Thr	CTA Leu	GCA Ala	TTA Leu	TTA Leu	CAC His	GAT Asp	TAT Tyr	TTT Phe	ACT Thr	GAA Glu	TCG Ser	CCT Pro	CGT Arg	965
				300				305					310				
70	CCT Pro	ACT Thr	GAC Asp	CCG Pro	AAA Lys	AAG Lys	TTG Leu	CCT Pro	AAA Lys	AAG Lys	TCT Ser	TCT Ser	CCA Pro	GAA Glu	AAG Lys	AGA Arg	1013
			315				320						325				
75	GAA Glu	AAT Asn	GAA Glu	GAT Asp	GAA Glu	CAG Gln	AAT Asn	AAT Asn	GGC Gly	TCT Ser	AAA Lys	AGA Arg	AGG Arg	CAT His	GTT Val		1058

330

335

340

TAGGTTTCTA TA

1070

5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25	TGT TCA GCT ATT GAT ACG AAA AGT TCA GTC TCA GCG ATG GAG CAC AAG	48
	Cys Ser Ala Ile Asp Thr Lys Ser Ser Val Ser Ala Met Glu His Lys	
	1 5 10 15	
30	ATT GCT ATA AAG AAA GTA ACA AAG ATT TTC AAC AAA GAC ATC CTT CTA	96
	Ile Ala Ile Lys Lys Val Thr Lys Ile Phe Asn Lys Asp Ile Leu Leu	
	20 25 30	
35	ATC AGG GCA ATA CGA GAG CTT AAG TTC ATG ATG TTT TTC AGA GGC CAC	144
	Ile Arg Ala Ile Arg Glu Leu Lys Phe Met Met Phe Phe Arg Gly His	
	35 40 45	
40	AAG AAT ATT GCA ACT TTG CTT GAC TTA GAT GTT GTA TAT GTG AAG CCT	192
	Lys Asn Ile Ala Thr Leu Leu Asp Leu Asp Val Val Tyr Val Lys Pro	
	50 55 60	
45	TAT GAA GGC TTG TAT TGT TTT CAA GAG CTA GCC GAT TTA GAT TTA GCT	240
	Tyr Glu Gly Leu Tyr Cys Phe Gln Glu Leu Ala Asp Leu Asp Leu Ala	
	65 70 75 80	
50	CGT GTT TTG TAC TCA AAC GTC CAA TTT TCA GAA TTT CAC ATT CAA AGC	288
	Arg Val Leu Tyr Ser Asn Val Gln Phe Ser Glu Phe His Ile Gln Ser	
	85 90 95	
55	TTT ATG TAC CAA ATT CTT TGC GGA CTC AAG TAC ATC CAT TCT GCT GAT	336
	Phe Met Tyr Gln Ile Leu Cys Gly Leu Lys Tyr Ile His Ser Ala Asp	
	100 105 110	
55	GTA ATA CAT CGG GAC CTA AAG CCA GGA AAC ATA TTG GTC ACC ACT CAA	384
	Val Ile His Arg Asp Leu Lys Pro Gly Asn Ile Leu Val Thr Thr Gln	
	115 120 125	
55	GGG ACT TTA AAA ATA TGT GAT TTC GGC TTA GCA CGA GGA ATA AAT CCT	432
	Gly Thr Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Gly Ile Asn Pro	
	130 135 140	

330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

GTA TAT TTC AGA AAC CGC TCA GCT GTC ATC ACA AAC TAC GTA GCA
Val Tyr Phe Arg Asn Arg Ser Ala Val Ile Thr Asn Tyr Val Ala
145 150 155

477

5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Thr Glu Val Val Ser Lys Ser Ser His Ser Phe Phe Asn Asn Leu
1 5 10 15
His Leu Ala Thr Ser Thr Ala Ser Ser Ser Val Ser Ser Thr Thr Pro
20 20 25 30
Lys Ile Glu Phe Asn Ser Ile Ala Glu Asn Asp Asp Ile Pro Thr Asn
35 40 45
Tyr Asp Ser Asp Glu Glu Phe Glu Asp Gly Asp Thr Phe Ile Gln Ser
50 55 60
Thr Leu Ile His Gln Phe Asn Ala Ser Gln Val Thr Thr Thr Thr Ile
30 65 70 75 80
Ile Ile Ile Pro Met Met Val Thr Thr Ile Ile Tyr Leu Gln Lys Leu
85 90 95
Asp Gly Ser Thr Pro Cys Thr Lys Pro Ile Lys Arg Leu His Arg Thr
35 100 105 110
Asn Phe Met Lys Ile Ile His Phe Glu Ile Tyr Asn Ile Glu Tyr Ser
115 120 125
His Leu Glu Ser Asp Leu Leu Pro Arg Ile Asp Ala His Gln Leu Ala
40 130 135 140
Arg Ile Leu Arg Gly Asp His Asp Asp Gln Phe Asp Glu Phe Ile Ile
45 145 150 155 160
Ile Asp Cys Arg Phe Glu Tyr Glu Phe Asn Gly Gly His Ile Thr Arg
165 170 175
Ala Ile Asn Ile Ser Thr Gln Glu Ala Leu Gln Glu Lys Leu Phe Gln
50 180 185 190
Tyr Gln Glu Thr Asp Thr Lys Asp Thr Glu Ser Lys Lys Arg Leu Ile
195 200 205
Ile Phe His Cys Glu Phe Ser Met Phe Arg Gly Pro Met Met Ala Lys
55 210 215 220
His Leu Arg Lys Cys Asp Arg Met Cys Asn Tyr Asp Asn Tyr Pro Leu

	225	230						235						240			
5	Leu	Thr	Tyr	Pro	Asp	Ile	Ala	Ile	Leu	Glu	Gly	Gly	Tyr	Lys	Asn	Phe	
					245					250				255			
	Tyr	Glu	Asn	Tyr	Pro	Gln	Trp	Cys	Asp	Pro	Gln	Gly	Tyr	Val	Glu	Met	
					260					265				270			
10	Lys	Asn	Leu	Arg	His	Lys	Lys	Leu	Cys	Glu	Ser	Asn	Leu	Asp	Lys	Val	
					275					280				285			
	Arg	Lys	Asp	Asn	Lys	Leu	Thr	Arg	Ala	Lys	Ser	Tyr	Gln	Phe	Gly	Ile	
					290					295				300			
15	Gln	His	Arg	Arg	Gly	Gly	Ser	Thr	Gly	Gly	Leu	Phe	Gly	Asn	Tyr	Asn	
					305					310				315			
	Tyr	Asn	Val	Met	Asn	Ser	Ser	Asp	Gln	Gln	Phe	Trp	Ser	Ser	Ser	Thr	
					325					330				335			
20	Ser	Asn	Thr	Ala	His	His	Arg	Ser	Ser	Ser	Ser	Ser	Gly	Phe	Ile	Asn	
					340					345				350			
	Asn	Met	His	Ser	Gly	Ala	Ser	Ser	Tyr	His	His	Arg	Ser	Gln	Ser	Phe	
					355					360				365			
	Val	Thr	Ile	Asn	Asn	Glu	Lys	Ile	Ile	Lys	Arg	Gln	Arg	Ser	Thr	Pro	
					370					375				380			
30	Lys	Val	Ser	Asn	Ser	Pro	Thr	Lys	Pro	Pro	His	Gln	Leu	Tyr	Leu	Leu	
					385					390				395			
	Ile	Asn	Pro	Phe	Arg	Trp	Leu	Ile	Phe	Ile	Asp						
					405					410							

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

50	Met	Thr	Lys	Pro	Arg	Phe	Leu	Thr	Arg	Tyr	Arg	Lys	Ser	Lys	Ser	Val
	1				5					10					15	
	Gly	Ile	Ser	Asp	Met	Ile	His	Tyr	Ser	Pro	Arg	Tyr	Ser	Asp	Asp	Ser
				20					25					30		
55	Tyr	Glu	Tyr	Arg	His	Val	Met	Leu	Pro	Lys	Asn	Met	Leu	Lys	Ala	Ile
			35					40					45			
	Pro	His	Asp	Tyr	Phe	Asn	Gln	Glu	Thr	Gly	Thr	Leu	Arg	Ile	Leu	Thr
		50					55					60				

Phe Pro Gly Asp Ser Glu Ile Asp Glu Ile Phe Arg Ile Phe Arg Ile
210 215 220

5 Leu Gly Thr Pro Asn Glu Glu Ile Trp Pro Asp Val Asn Tyr Leu Pro
225 230 235 240

Asp Phe Lys Ser Ser Phe Pro Gln Trp Lys Lys Lys Pro Leu Ser Glu
245 250 255

10 Ala Val Pro Ser Leu Asp Ala Asn Gly Ile Asp Leu Leu Asp Gln Met
260 265 270

15 Leu Val Tyr Asp Pro Ser Arg Arg Ile Ser Ala Lys Arg Ala Leu Ile
275 280 285

His Pro Tyr Phe Asn Asp Asn Asp Asp Arg Asp His Asn Asn Tyr Asn
290 295 300

20 Glu Asp Asn Ile Gly Ile Asp Lys His Gln Asn Met Gln
305 310 315

(2) INFORMATION FOR SEQ ID NO:10:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35 Met Pro Gln Val Thr Lys Thr Asn Asn Glu Asn Glu Phe Arg Leu Thr
1 5 10 15

Arg Ser Lys Val Gln His Gln Glu Ser Ile Ser Thr Ile Lys Asn Thr
20 25 30

40 Thr Ile Ser Asn Ser Gln His Lys Gln Gln Thr Gln Gln Gln Ile Ser
35 40 45

45 Ser Pro Pro Gln Val Ser Val Thr Ser Ser Glu Gly Val Ser His Val
50 55 60

Asn Thr Arg Gln Tyr Leu Gly Asp Val Ser Asn Gln Tyr Ile Thr Asn
65 70 75 80

50 Ala Lys Pro Thr Asn Lys Arg Lys Pro Leu Gly Gly Asp Asn Ala Pro
85 90 95

Leu Gln Lys Gln Gln His Arg Pro Ser Arg Pro Ile Pro Ile Ala Ser
100 105 110

55 Asp Asn Asn Asn Asn Gly Ser Thr Ser Ser Ser Ser Asn Ser Ser Asn
115 120 125

Asn Asn Asn Asn Asp Ala Asn Arg Leu Ala Ser Leu Ala Val Pro Ser

	130		135		140											
5	Arg 145	Leu	Pro	Gln	Lys	Arg 150	Gln	Ala	Thr	Glu	Ser 155	Ser	Thr	Asn	Leu	Val 160
	Glu	Lys	Leu	Arg	Val 165	Pro	Gln	Pro	Glu	Val 170	Gly	Glu	Arg	Ser	Gln	Ser 175
10	Tyr	His	Lys	Lys 180	Ser	Arg	Leu	Ile	Asp 185	Tyr	Glu	Trp	Gln	Asp 190	Leu	Asp
	Glu	Glu	Asp 195	Asn	Asp	Asp	Gln	Leu	Met 200	Val	Ser	Glu	Tyr 205	Val	Asn	Glu
15	Ile	Phe	Ser	Tyr	Tyr	Tyr	Glu 215	Leu	Glu	Thr	Arg	Met 220	Leu	Pro	Asp	Pro
20	Gln 225	Tyr	Leu	Phe	Lys	Gln 230	Thr	Leu	Leu	Lys	Pro 235	Arg	Met	Arg	Ser	Ile 240
	Leu	Val	Asp	Trp	Leu	Val	Glu	Met	His	Leu 250	Lys	Phe	Lys	Leu	Leu	Pro 255
25	Glu	Ser	Leu	Phe 260	Leu	Ala	Val	Asn	Val 265	Met	Asp	Arg	Phe	Met	Ser	Val
	Glu	Val	Val	Gln	Ile	Asp	Lys	Leu	Gln 280	Leu	Leu	Ala	Thr 285	Ala	Ala	Leu
30	Phe	Thr	Ala	Ala	Lys	Asn	Glu 295	Glu	Val	Phe	Ser	Pro 300	Leu	Val	Lys	Asn
35	Tyr 305	Ala	Tyr	Phe	Thr	Asp 310	Gly	Ser	Tyr	Thr	Pro 315	Glu	Glu	Val	Val	Gln 320
	Ala	Glu	Lys	Tyr	Met	Leu	Thr	Ile	Leu	Asn 330	Phe	Asp	Leu	Asn	Tyr	Pro 335
40	Asn	Pro	Met	Asn 340	Phe	Leu	Arg	Arg	Ile	Ser	Lys	Ala	Asp	Asp 350	Tyr	Asp
	Val	Gln	Ser	Arg	Thr	Leu	Gly	Lys 360	Tyr	Leu	Leu	Glu	Ile 365	Thr	Ile	Val
45	Asp 370	Tyr	Lys	Phe	Ile	Gly	Met 375	Arg	Pro	Ser	Leu	Cys 380	Cys	Ala	Leu	Ala
50	Met 385	Tyr	Leu	Ala	Arg	Leu	Ile	Leu	Gly	Lys	Leu 395	Pro	Val	Trp	Asn	Gly 400
	Asn	Leu	Ile	His	Tyr 405	Ser	Gly	Gly	Tyr	Arg 410	Ile	Ser	Asp	Met	Arg	Glu 415
55	Cys	Ile	Glu	Leu	Met	Phe	Gln	Tyr	Leu 425	Ile	Ala	Pro	Ile	Glu 430	His	Asp
	Glu	Phe	Phe	Lys	Lys	Tyr	Ala	Met 440	Arg	Lys	Phe	Met	Arg	Ala	Ser	Thr 445

Leu Cys Arg Asn Trp Ala Lys Lys Phe Gln Ala Ser Gly Arg Asp Leu
 450 455 460

5 Phe Asp Glu Arg Leu Ser Thr His Arg Leu Thr Leu Glu Asp Asp Asp
 465 470 475 480

Glu Glu Glu Glu Ile Val Val Ala Glu Ala Glu Glu
 485 490

10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 343 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Thr Ala Ala Val Ala Thr Lys Pro Ser Val Thr Ser Lys Pro
 1 5 10 15

25 Ala Thr Lys Gln Val Leu Asn Tyr Thr Lys Glu Lys Lys Val Gly Glu
 20 25 30

30 Gly Thr Tyr Ala Val Val Tyr Leu Gly Lys Gln Ile Ser Thr Lys Arg
 35 40 45

Gln Ile Ala Ile Lys Glu Ile Lys Thr Gly Leu Phe Lys Asp Gly Leu
 50 55 60

35 Asp Met Ser Ala Leu Arg Glu Val Lys Tyr Leu Gln Glu Leu Lys His
 65 70 75 80

Pro Asn Val Ile Glu Leu Val Asp Val Phe Ser Ala Thr Asn Asn Leu
 85 90 95

40 Asn Leu Val Leu Glu Phe Leu Pro Cys Asp Leu Glu Val Leu Ile Lys
 100 105 110

45 Asp Lys Ser Ile Val Phe Lys Ser Ala Asp Ile Lys Ser Trp Leu Leu
 115 120 125

Met Thr Leu Arg Gly Ile His His Cys His Arg Asn Phe Ile Leu His
 130 135 140

50 Arg Asp Leu Lys Pro Asn Asn Leu Leu Leu Ala Pro Asp Gly Gln Leu
 145 150 155 160

Lys Ile Ala Asp Phe Gly Leu Ala Arg Ala Leu Val Asn Pro Asn Glu
 165 170 175

55 Asp Leu Ser Ser Asn Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu
 180 185 190

Leu Phe Gly Ala Arg His Tyr Thr Gly Ala Val Asp Ile Trp Ser Ile

195 200 205

5 Gly Ile Ile Phe Ala Glu Leu Met Leu Arg Ile Pro Tyr Leu Pro Gly
210 215 220

Lys Asp Asp Val Asp Gln Leu Asp Val Thr Phe Arg Ala Tyr Gly Thr
225 230 235 240

10 Pro Thr Glu Gln Ile Trp Pro Asn Val Ser Ser Leu Pro Met Tyr Asn
245 250 255

Ala Leu His Val Tyr Pro Pro Pro Ser Arg Gln Glu Leu Arg Asn Arg
260 265 270

15 Phe Ser Ala Ala Thr Glu Lys Ala Leu Asp Leu Leu Ile Ser Met Thr
275 280 285

Gln Leu Asp Pro Ser Arg Arg Cys Asp Ser Thr Leu Ala Leu Leu His
290 295 300

20 Asp Tyr Phe Thr Glu Ser Pro Arg Pro Thr Asp Pro Lys Lys Leu Pro
305 310 315 320

Lys Lys Ser Ser Pro Glu Lys Arg Glu Asn Glu Asp Glu Gln Asn Asn
325 330 335

Gly Ser Lys Arg Arg His Val
340

30 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

40 Cys Ser Ala Ile Asp Thr Lys Ser Ser Val Ser Ala Met Glu His Lys
1 5 10 15

45 Ile Ala Ile Lys Lys Val Thr Lys Ile Phe Asn Lys Asp Ile Leu Leu
20 25 30

Ile Arg Ala Ile Arg Glu Leu Lys Phe Met Met Phe Phe Arg Gly His
35 40 45

50 Lys Asn Ile Ala Thr Leu Leu Asp Leu Asp Val Val Tyr Val Lys Pro
50 55 60

Tyr Glu Gly Leu Tyr Cys Phe Gln Glu Leu Ala Asp Leu Asp Leu Ala
65 70 75 80

55 Arg Val Leu Tyr Ser Asn Val Gln Phe Ser Glu Phe His Ile Gln Ser
85 90 95

	Phe	Met	Tyr	Gln	Ile	Leu	Cys	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asp	
				100					105					110			
5	Val	Ile	His	Arg	Asp	Leu	Lys	Pro	Gly	Asn	Ile	Leu	Val	Thr	Thr	Gln	
			115					120					125				
	Gly	Thr	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Gly	Ile	Asn	Pro	
			130				135					140					
10	Val	Tyr	Phe	Arg	Asn	Arg	Ser	Ala	Val	Ile	Thr	Asn	Tyr	Val	Ala		
	145					150					155						
15	(2) INFORMATION FOR SEQ ID NO:13:																
	(i) SEQUENCE CHARACTERISTICS:																
	(A) LENGTH: 1019 base pairs																
	(B) TYPE: nucleic acid																
	(C) STRANDEDNESS: both																
20	(D) TOPOLOGY: linear																
	(ii) MOLECULE TYPE: cDNA																
25	(ix) FEATURE:																
	(A) NAME/KEY: CDS																
	(B) LOCATION: 1..1017																
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:																
	ATG	AAG	TTG	TCA	GAT	TAT	TAT	ATA	GAC	AAG	GAA	TTA	ATT	TAC	AAT	AGT	48
	Met	Lys	Leu	Ser	Asp	Tyr	Tyr	Ile	Asp	Lys	Glu	Leu	Ile	Tyr	Asn	Ser	
	1				5					10					15		
35	GCC	ATT	TCT	GAT	ATA	TAT	ACG	GCT	ATT	GAT	AAG	TTT	AAT	AAC	TTA	CCA	96
	Ala	Ile	Ser	Asp	Ile	Tyr	Thr	Ala	Ile	Asp	Lys	Phe	Asn	Asn	Leu	Pro	
				20					25					30			
40	GTA	TGT	CTT	AAA	ATA	GTT	GAT	GAA	GAT	TTC	AGT	CTT	CCA	CCA	CAT	TCA	144
	Val	Cys	Leu	Lys	Ile	Val	Asp	Glu	Asp	Phe	Ser	Leu	Pro	Pro	His	Ser	
			35					40					45				
45	ATC	CAT	CGA	GAA	ATT	TTT	ATA	CTT	AAA	ACT	TTG	AAA	CCA	CAT	CCA	AAC	192
	Ile	His	Arg	Glu	Ile	Phe	Ile	Leu	Lys	Thr	Leu	Lys	Pro	His	Pro	Asn	
		50					55					60					
50	ATA	ATT	GAA	TAT	TTT	AAT	GAT	CTT	AAA	ATT	TAT	GAT	GAT	GTT	ATA	TTA	240
	Ile	Ile	Glu	Tyr	Phe	Asn	Asp	Leu	Lys	Ile	Tyr	Asp	Asp	Val	Ile	Leu	
	65					70					75					80	
55	GTC	ACC	AAA	TTG	TAT	CGT	TAT	GAT	TTG	AGT	CAA	TTG	ATT	GAA	ATT	ACA	288
	Val	Thr	Lys	Leu	Tyr	Arg	Tyr	Asp	Leu	Ser	Gln	Leu	Ile	Glu	Ile	Thr	
					85					90					95		
60	AAA	TAT	TGT	AAA	CGA	ACA	ACA	CGA	TTT	ATT	TAT	GGT	ATT	AAT	GGT	AAT	336
	Lys	Tyr	Cys	Lys	Arg	Thr	Thr	Arg	Phe	Ile	Tyr	Gly	Ile	Asn	Gly	Asn	
				100					105					110			
65	CTT	GTT	AGT	AAT	CAA	TAT	ACA	CTT	GCT	AAT	GAA	ATT	GAA	GAA	AAA	GAT	384
	Leu	Val	Ser	Asn	Gln	Tyr	Thr	Leu	Ala	Asn	Glu	Ile	Glu	Glu	Lys	Asp	
			115					120					125				
65	ATC	AAA	TTA	TGG	TTA	AAA	TCA	ATG	AGT	TCA	GGA	CTT	GAA	TTT	ATT	CAT	432
	Ile	Lys	Leu	Trp	Leu	Lys	Ser	Met	Ser	Ser	Gly	Leu	Glu	Phe	Ile	His	

	130		135		140		
5	TCA CAA GGG ATA ATT CAT CGT GAT ATA AAA CCC AGT AAT ATT TTC TTT Ser Gln Gly Ile Ile His Arg Asp Ile Lys Pro Ser Asn Ile Phe Phe 145 150 155 160	480					
10	GCC CGG GAT GAT ATA ACA CAA CCG ATT ATT GGA GAT TTT GAT ATT TGT Ala Arg Asp Asp Ile Thr Gln Pro Ile Ile Gly Asp Phe Asp Ile Cys 165 170 175	528					
15	TAT GAT TTA AAA CTG CCA CCT AAA GAT GAA CCC CCT ATG GCG AAA TAT Tyr Asp Leu Lys Leu Pro Pro Lys Asp Glu Pro Pro Met Ala Lys Tyr 180 185 190	576					
20	ATT GAT GTA TCT ACA GGT ATT TAT AAA GCA CCA GAA TTG ATT CTT GGT Ile Asp Val Ser Thr Gly Ile Tyr Lys Ala Pro Glu Leu Ile Leu Gly 195 200 205	624					
25	ATA ACT AAT TAT GAA TAT GAA ATT GAT ATT TGG TCA TTG GGT ATA ATT Ile Thr Asn Tyr Glu Tyr Glu Ile Asp Ile Trp Ser Leu Gly Ile Ile 210 215 220	672					
30	TTG ACT GGT TTA TAT TCA GAA AAT TTT CAA AGT GTT TTA GTC AAA GAT Leu Thr Gly Leu Tyr Ser Glu Asn Phe Gln Ser Val Leu Val Lys Asp 225 230 235 240	720					
35	GAT AAA GAA TTG ACT AAT GAT TCT CAT GTT AGT GAT TTA TAT TTA TTA Asp Lys Glu Leu Thr Asn Asp Ser His Val Ser Asp Leu Tyr Leu Leu 245 250 255	768					
40	AAT CAA ATA TTT GAA AAT TTC GGT ACA CCC AAT TTA ACT GAT TTT GAA Asn Gln Ile Phe Glu Asn Phe Gly Thr Pro Asn Leu Thr Asp Phe Glu 260 265 270	816					
45	GAT GAA TTA TTT TGT GAT GAA TAT AAT AAT GAA AAC TTG CAT TTT AAA Asp Glu Leu Phe Cys Asp Glu Tyr Asn Asn Glu Asn Leu His Phe Lys 275 280 285	864					
50	AAA TTC AAT TTA CAA AAA TAT CCT AGA AAA GAT TGG GAT ATT ATT TTA Lys Phe Asn Leu Gln Lys Tyr Pro Arg Lys Asp Trp Asp Ile Ile Leu 290 295 300	912					
55	CCT CGA TGC AAT GAT GAT TTA ATG AAA GAA ATT TTT ACC AAG ATG ATT Pro Arg Cys Asn Asp Asp Leu Met Lys Glu Ile Phe Thr Lys Met Ile 305 310 315 320	960					
60	AGA TAT GAT CGA AGT AAA AGA ATA ACT TCT AAA GAA ATC TTA CAA TTA Arg Tyr Asp Arg Ser Lys Arg Ile Thr Ser Lys Glu Ile Leu Gln Leu 325 330 335	1008					
65	ATG TTG GAT TG Met Leu Asp	1019					

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Leu Ser Asp Tyr Tyr Ile Asp Lys Glu Leu Ile Tyr Asn Ser

[illegible]